

Fig. 1A

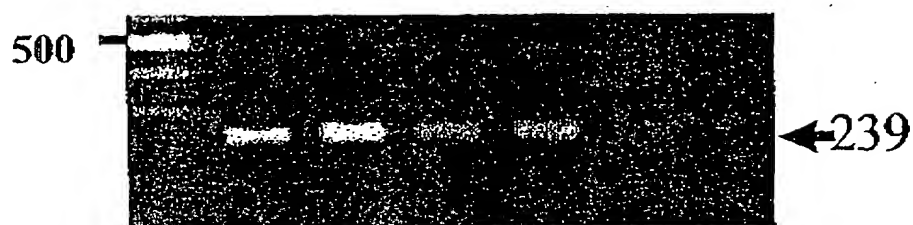


Fig. 1B

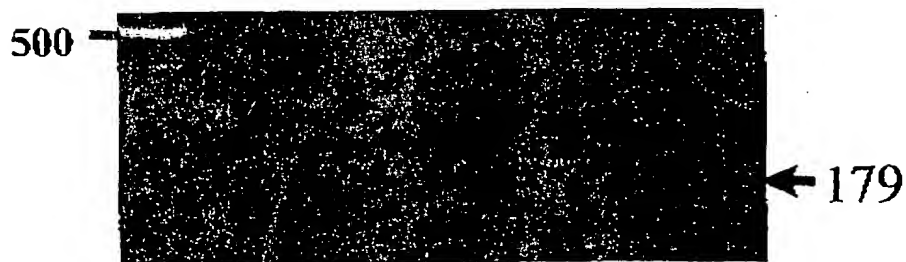


Fig. 1C

09973382.100901

09973382-100901
T0600T-285E7660

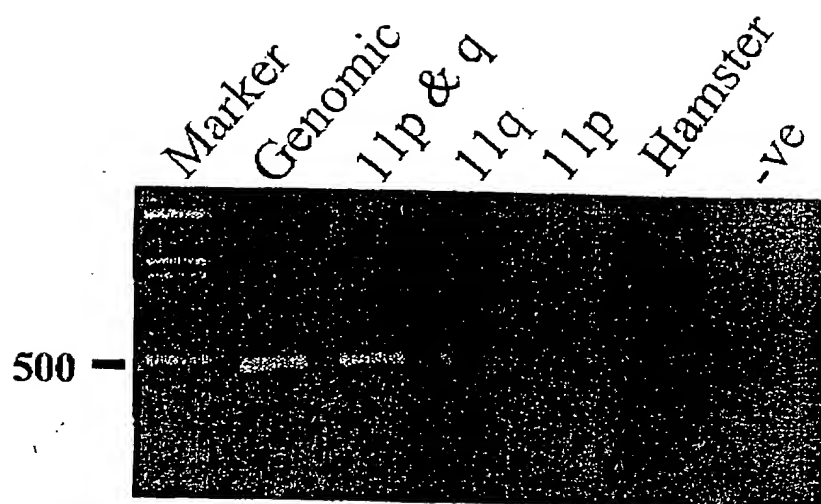


Fig. 2

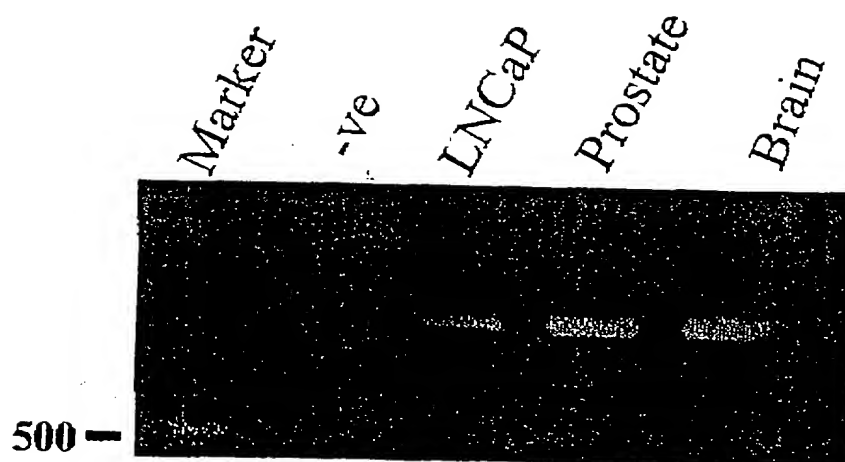


Fig. 3

09973382.100901

PSMA 1 MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFG 40
PSMA-LIKE 1 0

41 WFIKSSNEATNITPKHNMKAFLDELKAENIKKFLYNFTQI 80
1 0

81 PHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYP 120
1 0

121 NKTHPNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPP 160
1 0

161 FSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI 200
1 0

201 VIARYGKVFRGNKVNAQLAGAKGVILYSDPADYFAPGVK 240
1 0

241 SYPDGWNLPGGGVQRGNILNLNGAGDPLTPGYPANNEYAYR 280
1 0

281 RGIAEAVGLPSIPVHPIGYYDAQKLEKMGG SAPPDSSWR 320
1 MGG SAPPDSSWR 12

321 GSLKVPYNVGP GFTGNFSTQKV KMHIHSTNEVTRIYNVIG 360
13 GSLKVSYNVGP GFTGNFSTQKV KMHIHSTNEVTRIYNVIG 52

361 TLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVR 400
53 TLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVR 92

Fig. 4-1

10600T-28E2660

401 SFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSR 440
93 SFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSR 132

441 LLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKE 480
133 LLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKE 172

481 LKSPDEGFEGKSLYESWTKKSPSPEFSGMPRISKLGSGND 520
173 LKSPDEGFEGKSLYESWTKKSPSPEFSGMPRISKLGSGND 212

521 FEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYETYE 560
213 FEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYETYE 252

561 LVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY 600
253 LVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY 292

601 AVVLRKYADKIYSISMKHPQEMKTYSVSFDLSFSAVKNFT 640
293 AVVLRKYADKIYNISMKHPQEMKTYSLSFDLSFSAVKNFT 332

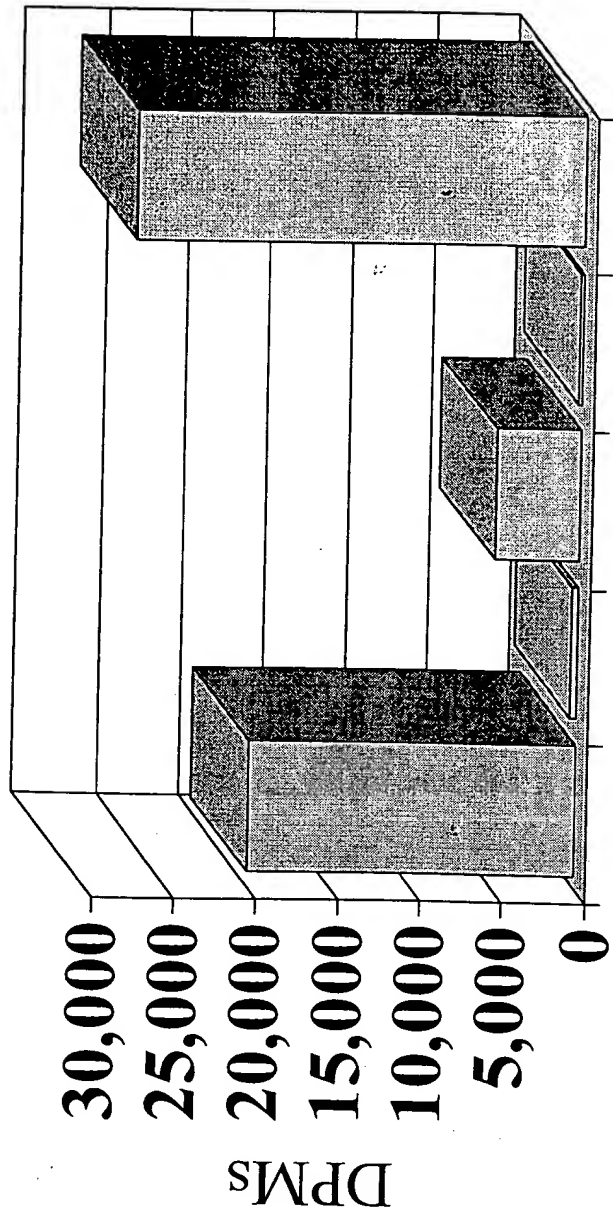
641 EIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLG 680
333 EIASKFSERLQDFDKSNPILLRMMNDQLMFLERAFIDPLG 372

681 LPDRPFYRHVIYAPSSH NKYAGESFPGIYDALFDIESKVD 720
373 LPDRPFYRHVIYAPSSH NKYAGESFPGIYDALFDIESKVD 412

721 PSKAWGEVKRQIYVAAFTVQAAAETLSEVA (SEQ ID NO: 4)
413 PSKAWGDVKRQISVAAFTVQAAAETLSEVA (SEQ ID NO: 2)

Fig. 4-2

FO6500T-28552660



total counts in rxn

Lysis alone

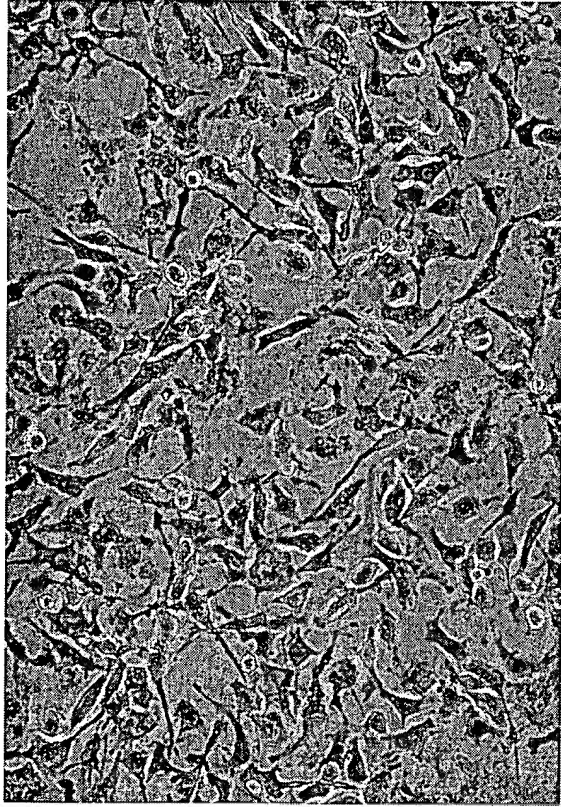
PC3-PSML

PC3-neo

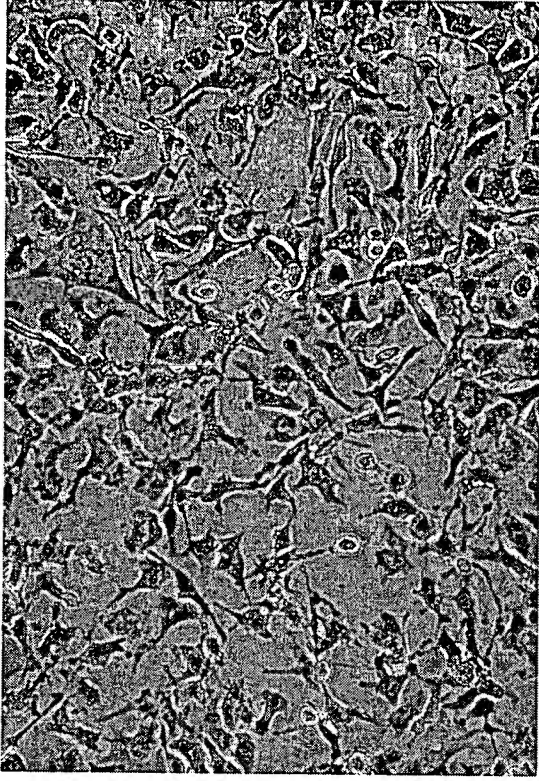
C4-2

FIG. 5

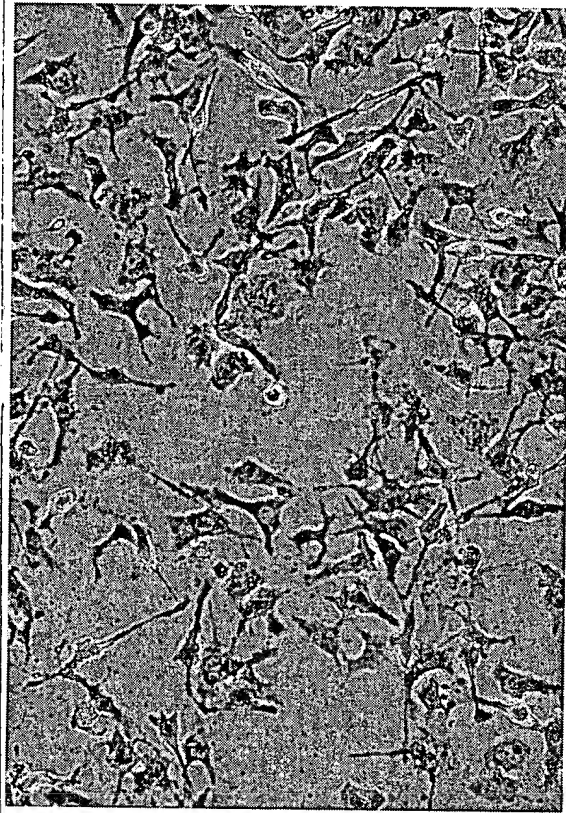
FO600T-28EEZ660



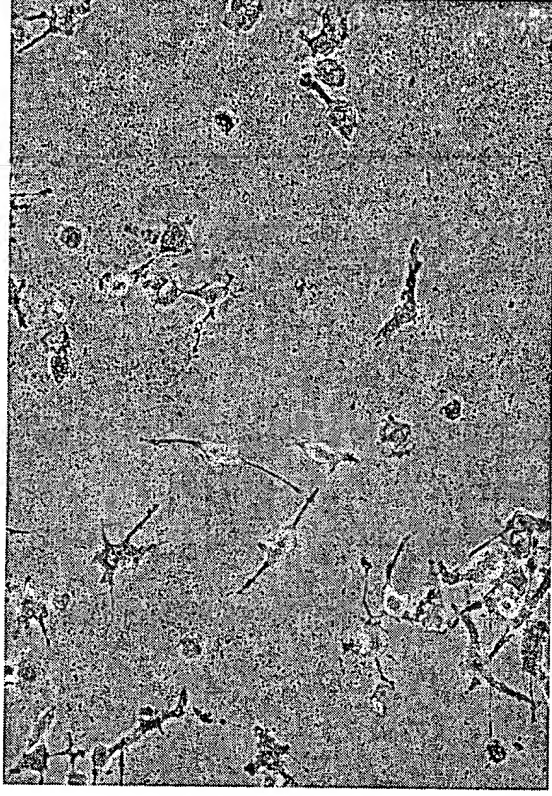
PC3-neo



PC3-PSMA



PC3-PSMA/Like Hybrid



PC3-PSM Like

Fig. 6